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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  834.5
343
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163.5
                                                                                                                                                                                              Score
                                                                                                                                                                          1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                  5:
6:
7:
9:
10:
11:
12:
13:
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                                                                                                                                                                                                       Query
                    62
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1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KRGCAGNFDSEERSSWYWGR.....SGCGXGLEVLFQGPVRKGXG 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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sp_bacteria:*
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                                                                                                                                                                                                                                                                                 sp_virus:*
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sp_vertebrate:*
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 239
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(without alignments)
1128.209 Million cell updates/sec
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               060593 homo sapien
060592 homo sapien
09uft2 homo sapien
042287 xenopus lae
035413 rattus norv
090788 schizosacch
09y338 homo sapien
099290 homo sapien
099290 rattus norv
                                                                          Q9u2t9 caeno
060593 homo
060592 homo
Q9uft2 homo
                                                                                                                                   Q9pull xenopus la
Q9ve96 drosophila
                                                                                                                                                      Q9nhc3
                                                                                                                                                                                            Description
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Q9yhu7 xenopus lae
Q9u2t9 caenorhabdi
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Q99059 avian
drosophila
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| 150.5 | 151 | 151 | 151.5 | 152 | 152.5 | 153 | 154 | 154.5 | 154.5 | 154.5 | 155 | 156 | 156.5 | 156.5 | 157 | 157 | 157 | 157 | 157.5 | 158 | 158 | 159 | 159 | 160 | 161 |
| 8.7 | 8.7 | 8.7 | 8.7 | | | æ | | | | 8.9 | | 9.0 | 9.0 | 9.0 | 9.1 | 9.1 | 9.1 | | | | | | | 9.2 | |
| 687 | 1186 | 1146 | 334 | 954 | 1011 | 1714 | 825 | 724 | 714 | 684 | 505 | 939 | 500 | 330 | 1696 | 1681 | 1676 | 1248 | 820 | 1220 | 1004 | 1721 | 1220 | 1721 | 1100 |
| 11 | Çī | 11 | σ | σı | ر. | 11 | 4 | 11 | 11 | 11 | ഗ | υ | σ | 4 | 4 | 4 | 4 | 4 | 11 | 4 | 4. | 4 | 4 | 4 | 4 |
| Q9QY53 | 061080 | Q9WVE1 | Q9TYT3 | 097180 | 061639 | Q9Z0R4 | 075815 | Q9Z0Z9 | Q9Z0Z8 | Q62417 | 097337 | Q24145 | Q9V5J3 | Q9NRB7 | Q9NZM3 | Q9NYG0 | Q9ULG4 | Q9NZM2 | Q9QZK2 | Q9UNK1 | Q9UHN7 | Q9UNK2 | Q9UET5 | 095216 | 094875 |
| Q9qy53 mus musculu | 061080 acanthamoeb | Q9wvel rattus norv | Q9tyt3 caenorhabdi | | 061639 drosophila | Q9z0r4 mus musculu | 075815 homo sapien | Q9z0z9 mus musculu | Q9z0z8 mus musculu | Q62417 mus musculu | 097337 paracentrot | Q24145 drosophila | Q9v5j3 drosophila | Q9nrb7 homo sapien | homo | homo | Q9ulg4 homo sapien | homo | Q9qzk2 mus musculu | Q9unk1 homo sapien | homo | Q9unk2 homo sapien | Q9uet5 homo sapien | homo | 094875 homo sapien |

ALIGNMENTS

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RESULT
Q9QW60
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                                                           Qy
                                                                                             Query Match
Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                      Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SMART; SM00326; SH3; 1.
SEQUENCE 239 AA; 26013 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9QW60 PRELIMINARY;
Q9QW60;
Q9QW60;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                  Margolis B., Silvennoinen O., Comoglio F., Roonprapunt C., Skolnik E., Ullrich A., Schlessinger J.; "High-efficiency expression/cloning of epidermal growth factor-receptor-binding proteins with Src homology 2 domains."; Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).
HSSP; Q64010; ICKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GRB-3-EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                    InterPro; IPR000980; -.
InterPro; IPR001452; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93028373; PubMed=1409582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp
65 INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS
                                 \omega
                                                               u
                                                 AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                 AGNFDSEERSSWYWGRLSRQEAVALLQGQRDGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                                                                              Conservative
                                                                                                                                                                           26013 MW;
                                                                                                          62.2%;
                                                                                             0;
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                                                                                             Score 1078; DB 11;
Pred. No. 1.7e-81;
0; Mismatches 1;
                                                                                                                                                                           48326D680C9F09B6 CRC64;
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                                                                                              Indels
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Best Local Similarity
Matches 159; Conserv
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DOMAIN
SEQUENCE
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DOMAIN
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NON_TER
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 11,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-90045469; PubMed-2554234;
MEDLINE-90045469; PubMed-2554234;
Tsuchie H., Chang C.H.W., Yoshida M.,
"A newly isolated avian sarcoma virus,
oncogene.";
                                                                                                                                                                                                                                                                                             PROSITE; PS50001; SH2; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                           Oncogene 4:1281-1284(1989).
-!- SIMILARITY: CONTAINS A EMBL; X17292; CAA35181.1; -HSSP; Q64010; 1CKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99059
                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAG-CRK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11957;
232
                  184
                                       172
                                                         124
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                                                                                                                                       σ
                                                                                       INSSGPRPPVPPSPAQP-PPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
                                                                                                                              AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPVPYVEKYRPASASVSALIGGNQEGS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIPVPYVEKCRPSSASVSTLTGG
          MIPVPYVEKYRPASASVSALIGG
                                               SRQGSGVILRQEEAEXVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM
                                       SRQNSGVILRQEEVEYVRALFDFNGNDDEDLPFKKGDILKIRDKPEEQWWNAEDMDGKRG
                                                                             VNSLGPAGGRRAGGEGPGAPGLNPTRFRIGDQEFDSLPSLLEFYKIHYLDTTTLIEPVSR
                                                                                                                    AGQFDSEDRGSWYWGRLSRGDAVSLLQRERHGTFLVRDSGSIPGDFVLSVSESSRVSHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sarcoma virus
                                                                                                                                                                                                                                                                                      SM00326;
                                                                                                                                                                                                                                                                                                                                                         IPR001452;
                                                                                                                                                                                                                                                                                                                                                                IPR000980; -.
                                                                                                                                                                                                                                                                            Polyprotein;
                                                                                                                                                                                                        <1
24
63
188
254
255
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                     SH3; 1.
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253
112
239
255
27985.
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                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                              COPY
                                                                                                                                                                                                                                                                            domain;
                                                                                                                                                         Score 834.5;
Pred. No. 2.5e
17; Mismatches
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                  206
                                                                                                                                                                                                         GAG (BY SIMILARITY).
CRK (BY SIMILARITY).
SH2 (OR B+C BOX) (BY SIMILARITY).
SH3 (OR A BOX) (BY SIMILARITY).
GAG (BY SIMILARITY).
; 0C562D0B2327A579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                  834.5;
No. 2.
                                                                                                                                                                                                                                                                             SH2
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, ASV-1, carries
                                                                                                                                                                                                                                                                             domain
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                                                                                                                                                         5; DB 14;
2.5e-61;
nes 26;
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on update)
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RESULT COPULT OF THE PROPERTY 
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Best Local S
Matches 93
                                                                                                                                                                                                             Q9PU11;
Q9PU11;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
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Q9NHC3;
Q9NHC3;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
SEQUENCE
                                                         Xenopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Ve.
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.

NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CED-2.
  SEQUENCE FROM N.A. Goisset C., Shi D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00401; SH2DOMAIN
PRINTS; PR00452; SH3DOMAIN
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF226866; AAF33845.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. elegans.";
Nat. Cell Biol. 0:0-0(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CED-2/CrkII and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00017; SH2; 1. Pfam; PF00018; SH3; 2.
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InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
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                                                                                                                                                                                              PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                         QPRLPAKAKUTFDRVPNAYDPTQLRVKKGQTVLVTQKMSNGMYKAELDGQIGSVPHTYLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPV 121
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C.,
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Similarity 31.0%;
93; Conservative !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AAYKKPIIEVVVGTFKFTGERETDLPFEQGERLEILSKTNQDWWEARNALGT
                                                                                                                                                                                                                0 (TrEMBLrel. 13, 0 (TrEMBLrel. 13, 1 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 16, Last annotation
ENGULEMENT PROTEIN CED-2.
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horvitz H.
and CED-10/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EDGTAAAGVKIANQSFPDIPALLNHFKMRVLTEASLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30878 MW;
    Boucaut J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I.R.;
/Rac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 343; DB 5;
Pred. No. 1.2e-20;
2; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KGASQSSIGSSGGGAERFSSASTSSDNIEL
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5CE7DA478948970B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phagocytosis
                                                                                                                                                                                                                                                                                                      217
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                                                                                                          Vertebrata;
a; Pipoidea;
                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111; Indels
                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                          Euteleostomi;
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
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                                                                                                                                                                                                                                                                                                                                                                                                              273
                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
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RESULT
Q9VE96
ID VE96
PT Q9
PT
RX MEDLINE-20196006: pubMed=10731132;

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Hardon R.G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Harlow R.M., Basu A., H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Ferriar S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferriar C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0499; P67PHOX.
PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VE96;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by interfering mutants of Sem-
Submitted (DEC-1997) to the EM
EMBL; AJ22361; CAB59279.1; -.
HSSP; P29354; 1GHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG7129 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VE96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000108; -.
InterPro; IPR000980; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001452; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Selective inhibition of neural induction but not mesoderm induction by interfering mutants of Sem-5/Grb2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTGMFPRNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRGMIPVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q---IFLRDIEQVPQQPTYVQALFDFDPQEDGELGFRRGDFIQVVDNSDPNWWKG-TCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGSGVILRQ-----EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYIEMKAHPWFFGKIPRAKAEEMLGKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00017; SH2; 1. PF00018; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 27.4
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00326; SH
CE 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AGKYFLWVVKFNSLNELVDYHR----STS----VSRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 213; DB 13;
Pred. No. 4.9e-10;
5; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2349A68260F9D4CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                  Miklos G.L.G.,
Baldwin D.,
Pasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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RESULT
Q9YHUG
ID QS
AC QS
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DT 01
DT 01
DT 01
DT 01
CC E1
OC E1
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibeqwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., San E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., San E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., San E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., San E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., San E.,
RA Shue B.C., Siden K., Wang X.,
RA Shue B.C., Siden K.,
RA Shue B.C., Siden K.,
RA Sh
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Best Local Similarity
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                 O9YHU6

O9YHU6;

O1-MAY-1999 (TrEMBLrel. 10, Created)

O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)

O1-MAY-1999 (TrEMBLrel. 16, Last annotation update)

O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)

PHOSPHOLIPASE C-GAMMA-1B (FRAGMENT).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 2.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003721; AAF55531.1; -. HSSP; P29354; IGFC.
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0038599; CG7129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000108;
                                                                                                                                                                                                                                                                                                                                587
                                                                                                                                                                                                                                                                                                                                                                             292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG
                                                                                                                                                                                                                                                                                                                                                                          THVRLLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYARVIQKRVPNAY-----DKTALALEVGELVKVTKINVSGQW-EGECNGKRGHFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEGIFPINYVDIKVPLGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSNGCQG---YMEEEVVPYAVALYDFDGIEPGDLSFREGEKIYLLDHPTPEWLRGRTRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGYAGSETPPSPPMPKGPPPPPPPPASSGGISLLDVINGKVDAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEP 120
                                                                                                                                                                                                                                                                                                                             --ANFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                         QQQLPTALCLYHFPGEVEGDLALQENELVTVL-YRINEDWLYGEVAGRQGQFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                      Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 200;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9E3EA36CC4A165A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAAAPTASAAAPSPSPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                               Euteleostomi;
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Best Local
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS50004; C2_DOMAIN_2; 1.
PROSITE: PS00018; EF_HAND; UNKNOWN_1.
PROSITE: PS50003; PH_DOMAIN; 1.
PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
PROSITE: PS50001; SH2; 2.
PROSITE: PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00390; PHPHLIPASEC. PRINTS; PR00401; SH2DOMAIN. PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1998)
EMBL; AF090112; AADO:
HSSP; P08487; 2PLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kung H.-F., Kim J., Huang
"Molecular cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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[1]
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##Pro; IPR000909; --
##Pro; IPR000980; --
##Pro; IPR001192; --
##Pro; IPR001192; --
##Pro; IPR001711; --
##Pro; IPR001849; --
##Pro; IPR002048; --
##Pro; IPR002048; --
##Pro; PF00018; SH3; 1.
##PF00168; C2; 1.
---YDKTALALEVGELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRESETFVGDYTLSFWRNGKVQHCRIHSRQEAGSPKLLLTDNLVFESLYALITHYQQMPL 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRDSSTSPGDYVLSVSENSRVSHYIINS----SGPR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSQANDDEEEQKEASNSSELHSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGAPDGSFL 455
                                                                                                                                                                                                EEQWWNAEDSEGKRGM-IPVPYVEK-YRPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGNFDSEER-----SSWYWGRL----SRQEAVALL-----QGQRHGVFL 39
                                                                     APRQDVHNGRPFVFTITGPQLNRYPLDVAADTLEDMQD---WIRKIREAAQTADARLTEG
                                                                                                                                                                  EGGWWRG-DCGGKKQMWFPANYVEEIFSPAEPEPERQNLDENSPLGDLLGGVLDVPSCHI
                                                                                                                                                                                                                                                              GTPDPDYGALYEGRNPGFYVEANPMPTFKCSVRALFDYKAQREDELTFTKNTIIQNVEKQ 695
                                                                                                                                                                                                                                                                                         SFRAEGKIKHCRVIQEGOSVVLGSSEFDSLVDLISYYEKHPMYRKMKLRYPINEETLEKI 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCNEFEMRLTEPVPQTNAHESKEWYHASLTRGQAEHMLMRVPRDGAFLVRKRSEQNSYAI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PPVPPSPAQ----
                                                                                                                  --NQEGSHPQP----LGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00387; PI-PLC-Y; 1. PF00388; PI-PLC-X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 21.7
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1067 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998) to the EMBL/GenBank/DDBJ databases AAD03595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.18; 21.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124019 MW;
                        267
                                                                                                                                                                                                                                                                                                                                                                                                       ---IGDQEFDSLPALLEFY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g Y.K., Lin
different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 193; DB 13;
Pred. No. 1.8e-07;
3; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533F6876ECDFE5DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PPPGVSPSRLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Xenopus phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123;
                                                                                                                                                                                                            -SASVSALIGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                       -KIHYLDTTTLIEPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity
                                                                                                                                                                                                                                                                      Pfam; PF00169; PH; 2.

Pfam; PF00189; PI-PLC-Y; 1.

Pfam; PF00388; PI-PLC-Y; 1.

Pfam; PF00388; PI-PLC-Y; 1.

PRINTS; PR00390; PHPHLIPASEC.

PRINTS; PR00678; PI3XINASEP85.

PRINTS; PR00401; SH2DOMAIN.

PRINTS; PR00401; SH2DOMAIN.

PROSITE; PS00004; C2_DOMAIN_2; 1.

PROSITE; PS500004; C2_DOMAIN; 1

PROSITE; PS50008; PIPLC_Y_DOMAIN; 1

PROSITE; PS50001; SH2; 2.

PROSITE; PS50001; SH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00017; SH2; 2
Pfam; PF00018; SH3; 1
Pfam; PF00168; C2; 1.
Pfam; PF00169; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHOLIPASE C-GAMMA-1A (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YHU7
Q9YHU7;
                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma-1.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF090111; AA
HSSP; P08487; 2PLD
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Kung H.-F., Kim J., Huang
"Molecular cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                     378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812
498 SFRAEGKIKHCRVIQEGQSVVLGSSEFDSLVDLISYYEKHPLYRKMKLRYPINEETLEKI
                                            438
                                                                                                                                318 GNQANDDEEEQKEASNSSELHSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGAPDGSFL
                       92
                                                                  72
                                                                                                 3 GCAGNFDSEER-----SSWYWGRL----SRQEAVALL-----QGQRHGVFL
                                                                                     VRESETFYGDYTLSFWRNGKYQHCRIHSRQEAGSPKFFLTDNLYFESLYALITHYQQMPL
                                          RCNEFEMRLTEPVPQTNAHESKEWYHASLTRGQAEHMLMRVPRDGAFLVRKRSEQNSYAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIMERRKKIALELSELV
                                                                                                                                                                                                                                                               SM00252;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PPVPPSPAQ----
                                                                                                                                                                                                                               1010 10
1010 AA;
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                               SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD03594.1;
                                                                                                                                                                                                                                          1010
                                                                                                                                                                                   10.6%;
                                                                                                                                                                                                                               116693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y.K., Lin
different
                      IGDQEFDSLPALLEFY --
                                                                                                                                                                         28;
                                                                                                                                                                                      Score 184.5; DB 1
Pred. No. 8.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                           Mismatches 101;
                                                                                                                                                                                                                               213247F73EE3EEDA CRC64;
                                                                M.C.;
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                                                                                                                                                                                                DB 13;
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                      -KIHYLDTTTLIEPV 121
                                                                                                                                                                                               Length 1010;
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; Pipidae;
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                                                                                                                                                                           Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                             Query
Best L
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO00108; -
InterPro; IPR000104; -
InterPro; IPR000261; -
InterPro; IPR000261; -
InterPro; IPR0002048; -
InterPro; IPR002048; -
Pfam; PF00018; SH3; 5.
Pfam; PF00036; efhand; 2.
PFAM; PF00036; efhand; 2.
PRINTS; PR00452; SH3;DOMAIN.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNPROSITE; PS0016; EF_HAND; UNKNOWN_2.
PROSITE; PS0018; EF_HAND; UNKNOWN_2.
SPROSITE; PS00018; EF_HAND; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018 (1998).
-!- SIMILARITY: TO EF-HAND FAMILY.
EMBL; ALI17204; CAB55138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y116A8C.36 PROTEIN.
Y116A8C.36.
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                         687
                                                                                                                                                                                                             627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLDENSPLGDLLGG
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  MPPNMTPSSSVDQIGVKAARKAEIAAA---
                                                                                                    RSEDELSFEPGDVIIVFQSHAAEPGWRAGQLREKVGWFPEAFVEAIAAVPTPGGDPPIQN 746
                                                                                                                                                                                                        GEFDKTDASQRFDADFGATSTADPFAQIAQAPAHSKGAVDQSAFNIHDTYKCRALFAFEA
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                                                  SPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEE
                                                                                                                                                                                                                                                                                                                 75; Conserv
                                                                                                                                                        STSPGDYVLSVSENS
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                            56;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                              Score 182; DB
Pred. No. 1.5e
56; Mismatches
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                                                                                                                                                        -RVSHY----- TINSSGPRPPVPP 76
                                                                                                                                                                                                                                                                                                                                          DB 5;
.5e-06;
MGLTEGGAPPASSAPAAAAVISQCI 798
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                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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Pfam; PF00208; Sorb; 1.
Pfam; PF00208; Sorb; 1.
PRINTS; PR00499; P67PHOX.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
01-AUG-1998
01-MAR-2001
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"ArgPB2, a multiple Src homology 3 domain-containing, Arg/Ab
"nteracting protein, is phosphorylated in v-Abl-transformed
localized in stress fibers and cardiocyte z-disks.";
J. Biol. Chem. 272:17542-17550(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           060593;
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Submitted (FEB-1998)
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SEQUENCE FROM N.A.
Colemis E.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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InterPro; IPR003127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97362243; PubMed=9211900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN 273
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                                                                                                          LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYYEKYRPASASYSALIGGNQEGSHP
                                                                                                                                                          TPEKEKLPA--
                                                                                                                                                                                      DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
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                                                                  LSFKKGDTVYILRKIDQNWYEGE-HHGRVGIFPISYVEKLTP
                                                                                                                                                                                                                                               SRTSPGRVDLPGSSTTLTKSF--TSSSPSSPSRAKDRESPRSYSSTLTDMGRSAPRERRG
                                                                                                                                                                                                                                                                                          SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP-----
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72; Conserv
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8 (TrEMBLrel.
1 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              ,; SH3; 1.
,40 640
.*. 70660 MW;
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Primates;
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16,
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                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGBP2B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                          Score 173;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 030A8C5036331674 CRC64;
                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             Length 640;
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                                                                                                                                                                                                                                                                                            ---PGVSPSRLRIG
                                                                                                                                                          -KAVYDFKAQTSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg/Abl-
                                                                                                                                                                                                                                                                                                                                    84;
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001452; ...
InterPro; IPR003127; ...
Pfam; PF00018; Sarb; 1.
Pfam; PF02208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PD016158; ...
PROSTITE; PS50002; SH3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-AUG-1998 (Tremburel 07, I
Ol-AUG-1998 (Tremburel 16, I
Ol-MAR-2001 (Tremburel 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  060592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang B., Golemis E.A., Kruh G.D.;
Submitted (FEB-1998) to the EMBL/
EMBL; AF049884; AAC05508.1; -.
HSSP; P29354; IGRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang B., Golemis E.A., Kruh G.D.;
"ArgBP2, a multiple Src homology 3 domain-containing, Arg/At interacting protein, is phosphorylated in v-Abl-transformed localized in stress fibers and cardiocyte Z-disks.";
J. Biol. Chem. 272:17542-17550(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00326; SH3; SEQUENCE 666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97362243; PubMed=9211900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                       537
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                                                                                                                                                                                                              QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN 273
                                                                                                                                                                                                                                                                                                                                                                TPEKEKLPA
                                                                    VDQNWYEGKIPGTNRQGIFPVSYVEVVKKNTKGAEDY
                                                                                                                                                                                                                                                                                        LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP
                                                                                                                  VSGQW-EGECNG--KRGHFPFTHVRLLDQQNPD-EDF 306
                                                                                                                                                                ----PEK---AQPA--RPPPPAQPGEI-GEAIAKYNFNADTNVELSLRKGDRVILLK-R
                                                                                                                                                                                                                                                                                                                                                                                                         DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRTSPGRVDLPGSSTTLTKSF--TSSSPSSPSRAKDRESPRSYSSTLTDMGRSAPRERRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP---
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                                                                                                                                                                                                                                                                 LSFKKGDTVYILRKIDQNWYEGE-HHGRVGIFPISYVEKLTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
72; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 173; DB 4; | Pred. No. 4.4e-06; 9; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B549A26DC04782E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666
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on update)
                                                                    573
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042287
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Best Local
                                                                                                                                                                                                       042287 PRELIMINARY;
042287;
01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-MAR-2001 (TrEMBLrel. 16, L
INTERSECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UFT2 PRELIMINARY; PRT; 816 AA.
Q9UFT2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 90.2 KDA PROTEIN.
  SEQUENCE FROM HOffman N.G.,
                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003127; -. Pfam; PF00018; SH3; 3. Pfam; PF02208; Sorb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koehrer K., Beyer A., Mewes
Submitted (SEP-1999) to the
EMBL; AL117472; CAB55947.1;
HSSP; Q60631; IGBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                      Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 816 AA; 90201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50002; SH3; 3
SMART; SM00459; Sorb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00459; P67PHOX. PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDENWYEGRIPGTSRQGIFPITYVDVIKRPLVKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSGQW-EGECNG--KRGHFPFTHVRLLDQ---QNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPLQKGDIVYIYKQIDQNWYEGE-HHGRVGIFPRTYIELLPPAEK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDSSTSPGDYVLSVSENSRVSHYIINSSGPRP-----PVPPSPAQPPPGVSPSRLRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001452; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Hardison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mewes
to the
  N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.W., Gassenhuber
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 170; DB 4; Pred. No. 1e-05;
     Yamabhai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFFE6647DC7730D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 100;
                                                                                                                                                                                                                                                                                                                                         1270
                                                                                                                                                        Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                         Ŗ
     Kay
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                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J., Wiemann databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213
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RESULT
035413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 75
InterPro; IRR00312; ...
InterPro; IRR003145; ...
InterPro; IRR003127; ...
InterPro; IRR003127; ...
Pfam; PF00018; SH3; 3.
Pfam; PF02208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PD016158; -; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001452; ...
InterPro; IPR002048; ...
Pfam; PP000018; SH3; 5
Pfam; PF00036; efhand; 2.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS00027; EH; 1.
SMARP; SM0027; EH; 1.
                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAR-2001 (TrEMBLrel. 16, Last annotation update)
SH3-CONTAINING PROTEIN P4015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO EF-HAND FAM
EMBL; AF032118; AAC73068.1; --
HSSP; P29355; 1SEM.
                                                                                                                           Ide N., Takeuchi M., Hata Y., Takai Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; AF026505; AAB81527.1; -
HSSP, P29354; IGRI.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                             035413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding.
SECTIONCE 1270 AA; 143670 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               035413;
                                                                                                                                                                                                                                                                                                                                                                                                                   1126
                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000261; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 EERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYIINSSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 KSTPTE 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNÄYDKTÄ----LALEVGELVKVTKINVSGQWEGE--CNGKR---GHFPFTHVRLL----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SYAATAPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTN 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EYI-SMYTYESNEQGDLTFQQGDLI-VVIKKDGDWWTGTVGE-KTGVFPSNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQQDMWWFGE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                           QQNPDE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RPKDSEAAG--SGGKTGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ASLKRVSSPAFK--PAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VQGQK-GWF-----PKSYVKLISGPLRKSTSIDSTSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 165; DB 13,
Pred. No. 4.7e-05;
                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EA940C1F6B6A6858 CRC64;
                                                                                                                                                                                                                                                                                                                                             1196
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                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKKPEIAQVIA---
                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                              Rattus
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Q9P7E8
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Query Match
Best Local S
Matches 57
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O9P7E8;
O1-CT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ACTIN BINDING PROTEIN WITH SH3 DOMAINS.
SAPAJ760.02C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryott: Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 57; Conser
                                                                                                                                                                                                                                                                                                                     STRAIN-972H:;

Harris D., Wood V., Rajandream M.A., Basumitted (MAR-2000) to the EMBL/GenBar EMBL; AL162631; CAB83085.1; -.

Interpro; IPR000108; -.
Interpro; IPR002108; -.
Interpro; IPR002195; -.
Pfam; PF00018; SH3; 2.
Pfam; PF00241; cofilin_ADF; 1.
Pfam; PF00241; cofilin_ADF; 1.
PRINTS; PR00472; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS500002; SH3; 2.
SMART; SM00102; ADF; 1.
SMORT; SM00102; ADF; 1.
SEQUENCE 857 AA; 91137 MW; 247EFA78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00326; SH3; SEQUENCE 1196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                       180
                                                                712
                                                                                                    124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292
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                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
GKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNG
                                                                                 SRQGSGVILRQEEAEYVR----ALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSE
                                                                                                                                                                                SGPRPP----VPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
                                                            --QVGGDVKATEHTQPTKTPAIVIYDYSPEEENEIELVENEQIQILEFVDDGWWLGENSK
                                                                                                                                         SVPQPPAAPVVPEVPSVPQPPAVPVVPEAGQLNEPVVPPLPPH-----DETQ--EP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYVEVVKRNTKGSEDY 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THVRLLDQQNP-DEDF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVQPGEI-GEAIAKYNFNADTNVELSLRKGDRIILLK-RVDQNWYEGKIPGTNRQGIFPV 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLONGPIYARVIOKRVPNAYDKTALALEVGELVKVTKINVSGQW-EGECNG---KRGHFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GE-HHGRVGIFPISYVEKLTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDLGRSVSRERRGTP---EKEVKLPAKAVYDFKAQTSKELSFKKGDTVYILRKIDQNWYE
                                                                                                                                                                                                                           l Similarity
57; Conser
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                            9.4%;
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                                                                                                                                                                                                                           35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                      Score 163.5; DB 3;
Pred. No. 3.7e-05;
5; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 164; DB 11;
Pred. No. 5.3e-05;
1; Mismatches 70;
                                                                                                                                                                                                                                                                                                                           247EFA78BAFE7097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PEK---AQPA--RPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                               857;
                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                              769
                                                                                                    179
                                                                                                                                           711
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Q9Y338
ID Q9Y338
AC Q9Y338
AC Q9Y338
AC Q9Y338
AC Q9Y338
DT 01-NOV
DT 01-NAR
DE SH3P12
OS HOMO S
OC EUKARY
OC MAMMANI
OC MAMANI
OC MAMARR;
OR SEQUEN
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                                                                        В
                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 163; DB 4; Length 684; Best Local Similarity 25.0%; Pred. No. 3e-05; Matches 67; Conservative 40; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SH3P12 PROTEIN.
HOMO Sapiens (Human).
EUKAryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-LIVER;
LIN W.S., Chuang L.M.;
Lin W.S., Chuang L.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF136380; AAD27647.1; -.
HSSP; Q60631; 1GBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y338
Q9Y338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000108; -.
InterPro; IPR001452; -.
InterPro; IPR001452; -.
InterPro; IPR001452; -.
Pfam; PF00018; SH3; 3.
Pfam; PF02208; Sorb; 1.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00492; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00326; SH3; 1.
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557
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                                                                                                                                                                                                                            425
                                                                                                                                                                                                                                                       101 PALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGD 160
                                                                                                                                                                                                                                                                                                   369 RESDGAPGD--LTSLENESQIYKSVLEGGVIPLQDLSGLKRPSSSASTKNSESPRHF--I 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            770 GQQGLFPSNYVE-----ITGPNETANNPP-'-----AEPQAGGP----
                                                                                                                                                                                                                                                                                                                                         41
GRIPGTSRQGIFPITYVDVIKRPLVKNP
                    GECNG--KRGHFPFTHVRLLDQ---QNP 302
                                                                                                          PGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQW-E 279
                                                                                                                                                PA-----DYLEST---EEFIRRRHD-----DKEMRPARAKFDFKAQTLKELPLQKGD 468
                                                                                                                                                                                                                                                                                                                                       RDSSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSL 100
                                                                        ----AQPKKLTPVQVLE----YGEAIAKFNFNGDTQVEMSFRKGERITLLR-QVDENWYE 556
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584
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Search completed: Job time: 178 sec

September

27, 2001, 16:43:10